



United States
Department of
Agriculture

Forest
Service

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January 13, 2015

Field Supervisor
Attention: Docket Number FWS-R8-ES-2014-0041
Fish and Wildlife Service
Pacific Southwest Region
1829 S. Oregon St.
Yreka, CA 96097

Dear Ms. Finley;

Thank you for the opportunity to be an independent peer reviewer for your proposed rule to list the West Coast Distinct Population Segment of the fishers as a threatened species under the U.S. Endangered Species Act. I also thank you for extending the time for me to complete this review.

First, I want to compliment the U.S. Fish and Wildlife Service (hereafter USFWS or Service) on the extensive detail and care clearly demonstrated in compiling information on this species. Over 500 sources from reports to peer reviewed publications were examined, summarized, and used to make an informed decision. The background work presented in the draft species report helped me understand the logic behind the decisions that were ultimately made in the proposed rule. Overall, this was an excellent package put together by the Service and its biologists.

My comments on both documents are outlined below. While I read the entire draft species report and proposed rule, I will largely (but not exclusively) limit my comments to where I have the most expertise, which is in the field biology and population genetics of fishers. Hopefully these comments and the additional information provided can help the Service as they proceed to evaluate the West Coast Distinct Population Segment of fishers.

Comments:

- 1) **Order.** I would have liked to see the alternatives to the Distinct Population Segment (DPS) earlier in the document. It was not until the end that I realized that the USFWS was considering other alternatives to a single DPS for the West Coast Fisher. It seems like this decision needs to be firmly made before any additional decisions regarding the biological status of the species are considered. This becomes apparent when thinking about small population dynamics (one of the threats that the Service is concerned about). If this is a single DPS then the cumulative population size and effective population size is larger and the threat to extinction diminished, whereas if the species was divided into multiple DPSs I would express much graver concern about a Southern Sierra Nevada (SSN) DPS and its likely ability to persist into the future. I offer my professional opinion regarding the DPS options below based on published and unpublished data from our genetics laboratory.



- 2) **DPS Alternative 1 and 2 - leaving out the Southern Oregon Cascade (SOC) reintroduced non-native population.** The origin of the SOC population is correctly identified on page 37 of the draft species report. These animals were reintroduced from British Columbia (BC) and Minnesota stock. Drew et al. (2003) show that all mitochondrial DNA (mtDNA) haplotypes are either haplotype 9 or haplotype 10, haplotypes common in BC and Minnesota. Meanwhile, the Northern California and Southern Oregon (NCSO) population was identified by Drew et al. (2003) as having either a haplotype 1 or 2. I agree with the Service that this suggests that these two populations have not become panmictic and are not interbreeding. However, in our genetics work with the USDI BLM we have identified one individual male fisher that was sampled East of I5, but grouped with the NCSO fishers and BLM samples collected West of I5. The analysis was based on 11 microsatellite (nuclear DNA) markers (Contact BLM – Medford Office for details and a copy of a July 2012 report). This sample collected East of I5 was also a haplotype 1 which is consistent with belonging to the NCSO. A second sample collected East of I5 did not have adequate DNA for microsatellite analysis or sex analysis but also had a haplotype consistent the NCSO. I believe this was the first time since we began studying the genetics of fishers around NCSO / SOC (starting in 2008) that a fisher from NCSO was identified close to the SOC population with no immediately identifiable barriers between it and the SOC fishers. This singular observation suggests that the NCSO population is expanding beyond the boundary of the currently proposed alternatives for the West Coast DPS. Given that native fishers are now documented extending East beyond I5, close to where introduced fishers have been observed (see Figure 3 in the proposed rule and Figure 7 in the draft species report), it seems like the proposed boundary should be reconsidered to include the SOC. Over the 40 year time horizon that the Service is using for the fisher, it is possible that these populations will grow together and could become indistinguishable.
- 3) **Support for DPS Alternative #2.** The Service reviewed the recent molecular genetic information that has been published, but doesn't seem to use this information in making decisions regarding DPS designations. Molecular genetic information from Drew et al. (2003) suggested that the NCSO and SSN populations of fishers may have been connected in recent-historical times (meaning within the last thousands of years). However, more recent papers from my program - Knaus et al. (2011), Tucker et al. 2012 [PLOS], Tucker et al. 2013 [Conservation Genetics], Tucker et al. 2013 [Dissertation], and Tucker et al. In Review [Molecular Ecology] all point towards longer term isolation of the NCSO and SSN.

Drew et al. (2003) used the appropriate technology of the time and examined ~301 base pairs of mtDNA to draw their conclusion that haplotype 1 was present in the NCSO and SSN suggesting connectivity. However, Knaus et al. (2011) clearly showed that when 16,290 base pairs of mtDNA (the entire mitochondrial genome) was examined, haplotype 1 in NCSO was very different than haplotype 1 in the SSN. By analogy, 301 base pairs allowed researchers to say both populations had something that was grey and had a small

tail, whereas using the entire mitochondrial genome allowed us to realize that we were looking at an elephant and a mouse. Using some very basic molecular clock assumptions Knaus et al. (2011) show that this separation between the SSN and NCSO is consistent with being thousands of years old. Tucker et al. (2012, 2013 [PLOS]) follow up on this result with research using nuclear DNA markers and come to similar conclusions. Tucker et al. (2013) show that the fishers distribution in California (NCSO and SSN) contracted to the two current areas pre-European settlement. Tucker et al. (2012) also used museum specimens to confirm that the isolation of the SSN was not recent and to show that this isolation has continued, and possibly intensified. Tucker et al. (2012) speculate that a Medieval Climate Anomaly known as the Medieval Warm Period may have created mega-droughts that effectively severed connectivity in the Sierra Nevada for fishers, and other species such as wolverine, foxtail pine, and great grey owls. The main point is that populations in the NCSO and the SSN have been markedly separate for a long period of time. There is also evidence from Knaus et al. (2011) that there has been adaptive divergence among these populations creating significant evolutionary trajectories.

- 4) **Unpublished Historical and Contemporary Genetics Analysis.** Our genetics program has worked with several collaborators to examine both historical and contemporary genetic fisher samples along the West Coast of North America. We have conducted both nuclear and mitochondrial DNA research. We will be publishing this information soon. We first examined 859 fisher samples with 10 microsatellite (nuclear) DNA markers from British Columbia, SOC, NCSO, the Cascades (historical), the Olympic Peninsula (historical), and the SSN. We used two common approaches to examine population substructure: program STRUCTURE (Pritchard et al. 2000) and a principal coordinates analysis (PCA).

The STRUCTURE analysis suggests that most supported division of the samples is between the Sierra Nevada and the remainder of the samples. This is consistent with the results from Tucker et al. (2012) and Knaus et al. (2011). The next most supported break separates “Northern” samples. This includes samples from both East and West of the Rocky Mountains in British Columbia, historical samples from Alberta, SOC samples (reintroduced largely from British Columbia), and historical and contemporary samples from the Olympic Peninsula. However, this second break is less supported than the first division. Overall, this comprehensive analysis suggests that the SSN is a well-supported DPS, with the second DPS being everything north of the SSN. It also supports the NCSO being managed as a separate management unit (although not necessarily a DPS) from the reintroduced populations with BC origins. The PCA results largely mirror the STRUCTURE results.

The published and unpublished genetic data support DPS alternative #2 and do not support DPS alternative #1.

- 5) **Consider using habitat use data at multiple spatial scales from the Rocky Mountains.** There are several papers from the Rocky Mountains that are important for understanding fisher distribution and habitat use. I believe the ideas in these papers support findings in the proposed rule. Below I outline several papers that the Service should be aware of:

Olson, L.E., et al. "Modeling the effects of dispersal and patch size on predicted fisher (*Pekania* [Martes] *pennanti*) distribution in the US Rocky Mountains." *Biological Conservation* 169 (2014): 89-98.

- This is a species distribution model that showed that fisher were more likely found in mesic forest types with tall trees, much rain, and mid-range winter temperatures.
- Two models were considered, one with traditional vegetation, topographic and climatic variables, and the other with only topographic and climatic variables. The topographic and climatic variable model was futured under two climate change scenarios and multiple dispersal scenarios. Dispersal without considering patch size limitations could increase fisher habitat by ~25% by 2090, yet dispersal limited by non-habitat areas and a minimum patch size could decrease habitat by ~26%.
- This paper supports many of the habitat associations from the West Coast DPS fisher, and recognizes the complexity of climate modeling for a species such as fisher. It also shows the importance of dispersal for fishers to be able to follow ecosystems with high climate velocity.

Schwartz, M.K., et al. "Stand and landscape-scale selection of large trees by fishers in the Rocky Mountains of Montana and Idaho." *Forest Ecology and Management* 305 (2013): 103-111.

- Fishers used stand sites and regional landscapes in late-successional forests with large diameter trees and without ponderosa or lodgepole pines. Fishers also selected more concave, mesic landscapes.
- Large trees are important yet so is variation in the stand. Most importantly the results suggest Rocky Mountain fisher habitat selection happens at multiple scales.

Sauder, J.D., and J.L. Rachlow. "Both forest composition and configuration influence landscape-scale habitat selection by fishers (*Pekania pennanti*) in mixed coniferous forests of the Northern Rocky Mountains." *Forest Ecology and Management* 314 (2014): 75-84.

- Fisher chose home-range landscapes with larger, more contiguous patches of mature forest and less open areas (fishers chose landscapes with >50% mature forest in connected, complex shapes with few isolated patches and open areas comprising <5% of the landscape).
- Landscapes managed for timber production and roadless/wilderness had more open areas, less mature forest, and reduced proximity of mature forest patches than occupied fisher home ranges.

- 6) **Data quality and SDMs.** Figure 2 and 3 in the draft species report are very interesting, but very different than other SDMs I have seen for fisher. I was unclear on what data were used to model fisher habitat as this model seems to predict more fisher habitat than I suspected for fishers, leading to an image that suggests high connectivity throughout their range. More details are needed on how this map was derived compared to the Spenser and Rustigian-Romsos (2012) report cited in the draft species report, and the Davis et al. (2007) *Ecological Applications* paper. The Davis et al. (2007) paper is also consistent with my suggestion above of adopting DPS alternative #2. I wondered if the modeled fisher habitat used all of the fisher records, or only the records with high reliability ratings. McKelvey et al. (2008) show 3 examples of problems using low reliability ratings (including an example with West Coast fishers).
- 7) **Use of northern spotted owl for predicting fisher habitat.** Because of the nuances with using a fisher model built in one area and applying it in another area (Davis et al. 2007), or with one quality dataset and applying it across the range (McKelvey et al. 2008), I was very uncomfortable with using northern spotted owl habitat data as a surrogate for fisher data unless there is a direct test of the hypothesis that northern spotted owl data predicts fisher habitat and use. Barring this statistical evaluation a surrogate should not be used. There are many new papers (e.g., Cushman et al. 2008, Lindenmayer and Likens 2011, and Schwartz et al. In Press) noting that surrogates, while appealing, should only be used once thoroughly investigated. Unless a clear statistical relationship between a surrogate measure such as spotted owl habitat and fisher distribution is established, I would not use northern spotted owls for fisher.
- 8) **Tucker et al. In Review.** I want to make the Service aware of a publication that is in a second round of review by Jody Tucker. The basic ideas of this paper can be found in Tucker et al. (2012 Dissertation). She found that factors that influenced gene flow and movement varied by sex. For female fishers dense forest was important for movement, whereas other variables (e.g., roads, water, canyons, etc.) were important for movement depending on region within the SSN. For males mixed conifer was important for movement although only weakly so. Few other variables influenced movement for males, suggesting a higher degree of mobility across landscapes.
- 9) **Small population dynamics.** I was pleased to see that both the proposed rule and the draft species report considered small population dynamics. However, the effects of small populations on genetic variation and persistence were largely ignored. Several of the Tucker et al. papers describe the genetic based problems associated with small populations that ultimately lead to demographic issues. If the Service considers DPS alternative #2 I hope they account for a recovery area large enough in the SSN to support a population of fishers that will not suffer the stochastic genetic and demographic effects of small populations. This may require expanding the current SSN northern boundary in alternative #2 further north.

I hope my comments are of use to the Service. If there are any questions, please don't hesitate to contact me via e-mail (mkschwartz@fs.fed.us) or phone (406-370-0976).

Sincerely,

A handwritten signature in black ink, appearing to read "Michael K. Schwartz". The signature is fluid and cursive, with the first name "Michael" being more legible than the last name "Schwartz".

Michael K. Schwartz, Ph.D.
Director, National Genomics Center for Wildlife and Fish Conservation